Supplemental Table S4: Characterization and classification of hypothetical and unclassified proteins in the proteome *C. neoformans* under regulation of Pka1.

Accession number	Target P ^a	TMH MM ^b	Signal P ^c	GPI- SOM ^d	ProtFun ^e	Homologues ^f
					Central intermediary	S
CNAG_00012	O	0	No	No	metabolism/Enzyme/-/-	NAD-binding protein
					Amino acid	
					biosynthesis/Enzyme/Lyase/Growth	
_CNAG_00275*	M	0	No	No	factor	NAD-binding protein
					Translation/Non-enzyme/-/Transcription	
CNAG_00286	O	0	No	No	regulation	NAD-binding protein
					Amino acid	
					biosynthesis/Enzyme/Lyase/Immune	
CNAG_00409	M	0	No	No	response	Methyltransferase type 11
					Regulation and transcription/Non-	
CNAG_00465	O	0	No	No	enzyme/-/Transcription regulation	RNA methylase
					Regulation and transcription/Enzyme/-	Translation initiation factor
CNAG_00520	O	0	No	No	/Transcription regulation	IF-2
					Regulatory functions/Non-enzyme/-	Mago-bind domain-
CNAG_00577	O	0	No	No	/Transcription	containing protein
CNAG_00626	M	0	No	No	Translation/Non-enzyme/-/Growth factor	Uncharacterized protein
					Central intermediary	
CNAG_00858	O	0	No	No	metabolism/Enzyme/Isomerase/-	RNA-binding protein
			Yes		Transport and binding/Enzyme/-/Growth	Meiotic recombination-
CNAG_00995	S	0	(20/21)	No	factor	related protein
					Translation/Enzyme/-/Voltage-gated ion	
CNAG_01052	M	0	No	No	channel	Uncharacterized protein
					Central intermediary metabolism/Non-	Mitochondrial zinc
CNAG_01089	M	0	No	No	enzyme/-/Structural protein	maintenance protein 1
					Purines and	
					pyrimidines/Enzyme/Ligase/Growth	Replication factor C subunit
CNAG_01222	M	0	No	No	factor	2
						Centromere-binding protein
CNAG_01317	O	0	No	No	Translation/Non-enzyme/-/Growth factor	1

Accession number	Target P ^a	TMH MM ^b	Signal P ^c	GPI- SOM ^d	ProtFun ^e	Homologues^f
					Regulatory functions/Enzyme/-	
CNAG_01375	O	0	No	No	/Transcription	Related to Drebrin F
CNAG_01446	O	0	No	No	Translation/Non-enzyme/-/Transcription	HSP12
CNAG_01644	О	0	No	No	Regulation and transcription/Non- enzyme/-/Transcription regulation	HAT family dimerization protein
CNAG_01743	0	0	No	No	Translation/Non-enzyme/-/Transcription regulation	Proteophosphoglycan ppg4
CNAG_01811	О	0	No	No	Translation/Non-enzyme/-/Growth factor	DUF1014-domain- containing protein
CNAG_01892	0	0	No	No	Energy metabolism/Enzyme/-/Growth factor	Uncharacterized protein
CNAG_02118	О	0	No	No	Replication and transcription/Enzyme/-/Transcription regulation	Uncharacterized protein
CNAG_02129	O	0	No	No	Translation/Enzyme/Ligase/-	DUF4449 family protein
CNAG_02145	M	0	No	No	Amino acid biosynthesis/Enzyme/-/Growth factor	50S ribosomal protein L28
CNAG_02263*	O	0	No	No	Energy metabolism/Enzyme/Isomerase/-	Glutathione S-transferase
CNAG_02335*	О	0	No	No	Translation/Enzyme/-/-	Genomic scaffold, msy-sf-12 protein
CNAG_02400	О	0	No	No	Replication and transcription/Enzyme/-/-	Proteasomal ubiquitin receptor adrm1-like
CNAG_02842	M	0	No	No	Translation/Enzyme/Lyase/Growth factor	50S ribosomal subunit L30
_CNAG_02843*	О	0	No	No	Central intermediary metabolism/Non-enzyme/-/Growth factor	Protein vip1
CNAG_02994	U	0	No	No	Purines and pyrimidines/Enzyme/-/Transcription regulation	Carbohydrate-binding module family 48 protein
_CNAG_03007	O	0	No	No	Translation/Enzyme/-/-	CipC protein
_CNAG_03038	О	0	No	No	Translation/Enzyme/Lyase/Growth factor	and domain-containing protein
CNAG_03058	0	0	No	No	Regulation and transcription/Non- enzyme/-/Transcription regulation	Hmp1 protein
CNAG_03143*	O	0	No	No	Translation/Non-enzyme/-/Hormone	12kDa heat shock protein

Accession number	Target P ^a	TMH MM ^b	Signal P ^c	GPI- SOM ^d	ProtFun ^e	Homologues ^f
						(Glucose and lipid-regulation
						protein)
					Translation/Non-enzyme/-/Transcription	Phosphatidylserine
CNAG_03566*	O	1	No	No	regulation	decarboxylase proenzyme
CNAG_03677	O	0	No	No	Amino acid biosynthesis/Enzyme/-/-	TRAPP domain protein
					Translation/Non-enzyme/-/Transcription	
CNAG_03688	O	0	No	No	regulation	Uncharacterized protein
					Regulatory functions/Non-enzyme/-	
CNAG_03705	O	0	No	No	/Growth factor	Uncharacterized protein
					Replication and transcription/Non-	
CNAG_03841	O	0	No	No	enzyme/-/-	Dsp1-1-like protein
					Regulatory functions/Enzyme/-/Growth	
CNAG_03864	O	0	No	No	factor	Protein tyrosine kinase
						Similar to MKL/myocardin-
CNAG_03873	0	0	No	No	Fatty acid metabolism/Enzyme/-/-	like protein 1
		_			Energy metabolism/Enzyme/-/Growth	
CNAG_03961	M	0	No	No	factor	Bcs1p-like protein
CD X 1 CO 0 11 CO 1			3.7			CsbD domain-containing
CNAG_04163*	O	0	No	No	Transport and binding/Non-enzyme/-/-	protein
					Purines and	
C) 1 4 C 0 4000			3.7		pyrimidines/Enzyme/Lyase/Growth	
CNAG_04203	O	0	No	No	factor	Uncharacterized protein
C) 1 1 C 0 1010			3.7		Cell envelope/Non-enzyme/-	DYIGH (OO I
CNAG_04212	O	0	No	No	/Transcription	DUG1690 domain protein
C) X 1 C			3.7		Regulation and transcription/Non-	T. 1. WYYYD 3 (D.T.
CNAG_04284	O	0	No	No	enzyme/-/Growth factor	Tudor/PWWP/MBT
CD 1 4 C 0 4 4 5 5 1		0	3.7			Phosphoglycerate mutase-
CNAG_04475*	O	0	No	No	Translation/Non-enzyme/-/Growth factor	like protein
CNAG_04680	M	0	No	No	Biosynthesis of cofactors/Enzyme/lyase/-	Uncharacterized protein
					Purines and	WD40 repeat-containing
CNAG_04954	0	0	No	No	pyrimidines/Enzyme/Ligase/Transcription	•
CNAG_04962	O	0	No	No	Cell envelope/Non-enzyme/-/Structural	Chromosome segregation

	Accession number	Target P ^a	TMH MM ^b	Signal P ^c	GPI- SOM ^d	ProtFun ^e	Homologues ^f
						protein	ATPase-like protein
						Energy metabolism/Enzyme/-/Growth	
C	NAG_05001	O	0	No	No	factor	Thioredoxin-like protein
						Energy metabolism/Enzyme/-/Growth	
_ <u>C</u>	NAG_05131	M	0	No	No	factor	Ixr1p
						Transport and binding/Enzyme/-/Immune	Carbohydrate-binding
<u>C</u>	NAG_05312	O	0	No	No	response	module family 13 protein
						Central intermediary	
C	NAG_05570	O	0	No	No	metabolism/Enzyme/-/-	Ubiquitin C variant
						Energy metabolism/Enzyme/-/Growth	
C	NAG_06109	O	0	No	No	factor	Uncharacterized protein
							Hyaluronan/mRNA-binding
	NAG_06113	O	0	No	No	Translation/Non-enzyme/-/Growth factor	protein
						Translation/Enzyme/Isomerase/Growth	
	NAG_06328	O	0	No	No	factor	Ycii-related domain protein
						Replication and transcription/Enzyme/-	Rnapii degradation factor
C	NAG_06475*	O	0	No	No	/Growth factor	def1
<u>C</u>	NAG_06577	M	0	No	No	Translation/Enzyme/-/-	Allergen
						Replication and transcription/Enzyme/-	Transcriptional repressor
_ <u>C</u>	NAG_06765	O	0	No	No	/Transcription regulation	LEUNIG (or GG17798)
						Regulatory functions/Non-enzyme/-	RanBP1 domain containing
_ <u>C</u>	NAG_07322	O	0	No	No	/Transcription regulation	protein
						Central intermediary	Mitochondrial ribosomal
_ <u>C</u>	NAG_07382*	M	0	No	No	metabolism/Enzyme/Lyase/-	small subunit protein Mrp51
						Regulatory functions/Enzyme/-/Growth	Histidine phosphatase family
_ <u>C</u>	NAG_07547	M	0	No	No	factor	containing protein
						Replication and transcription/Enzyme/-	
C	NAG_07665	O	0	No	No	/Transcription regulation	Uncharacterized protein
						Central intermediary	2,3-diketo-5-methylthio-1-
<u>C</u>	NAG_07740	O	0	No	No	metabolism/Enzyme/Lyase/-	phosphopentane phosphatase

^aTargetP (cut off > 0.9) predicts subcellular location, M: mitochondrion, O: other, U: unknown (value below cut-off). ^bTMHMM predicts transmembrane helices.

Note: Table S1 provides that abundance values for the proteins upon modulation of PKA expression.

^cSignalP predicts N-terminal signal peptide. ^dGPI-SOM predicts GPI-anchor proteins.

^eProtFun predicts protein function and enzymology.

^fHMMER predicts homologues.

*Significant proteins after multiple hypothesis testing (FDR < 0.05).